


Continuous Description of Discrete Biological Data: Algorithms Based on a Stochastic Flow Model

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ABSTRACT

The applicability of differential equations to description of integer values dynamics in bio-informatics is investigated. It is shown that a differential model may be interpreted as a continuous analogue of a stochastic flow. The method of construction of a quasi-Poisson flow on the base of multi-dimension differential equations is proposed. Mathematical correctness of the algorithm is proven. The system has been studied by a computer simulation and a discrete nature of processes has been taken into account. The proposed schema has been applied to the classical Volterra's models, which are widely used for description of biological systems. It has been demonstrated that although behaviour of discrete and continuous models is similar, some essential qualitative and quantitative differences in their dynamics take place.

KEYWORDS

Bioinformatics, Continuous Model, Differential Equation, Discrete Model, Mathematical Modelling, Poisson Flow, Volterra's Model

INTRODUCTION

Mathematical modelling, particularly, in bioinformatics, is a booming field, which is quite far from a steady state. Different approaches are in use, and it is not obvious, what mathematical tool is better in this or that case. The methods can even compete, although should complement each other. In the present article, a way of complex use of differential equations and stochastic flows are proposed.

The usage limits determination of continuous models is one of the topical problems of the mathematical biology. There is number of characteristics of biological systems' dynamics, producing the discrete effects: development and restructuring of biosystems, information interactions, etc. It is especially typical for bioinformatics, where all main indices, characterised studying systems, are discrete and, additionally, using computer tools is also based exclusively on discrete description.

In the same time, when one moves from data collection to dynamical modelling, it is very attractive to use such mathematical tool as differential equations. They provide the researcher by a range of possibilities of both quantitative and qualitative description of real processes. It is pure continuous description, but there is a way of its discretisation. Accounting of discrete nature of system parameters (phase co-ordinates), as it was mentioned above, leads to its discretisation for the time co-ordinate. The paper is concerned with the construction of correct method of the time discretisation, based on previous results of the author, starting from (Chernyshenko, 1989). The time step is considered as non-constant value; it depends on dynamic parameters of the system. As well

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known, discretisation decreases the system stability (Casti, 1979). The correct determination of the time step help to investigate specific phenomenon of real ecosystem dynamics such as loss of stability, pseudo-stochastic behaviour, etc.

BACKGROUND

The bioinformatics, as a field, includes a number of mathematical approaches to description of various aspects of biological systems' functioning (Bioinformatics..., 2013; Shen, Tuszynski, 2008). At the present time, two ways of modelling – by differential equations and by stochastic processes – are developing, mainly, independently. An observation of the approaches can be finding, particularly, in (Brown, Rothery, 1993; Erciyes, 2015; Kunita, 1986). In some meaning they are opposite ways: differential equations are continuous and, usually, deterministic models; and stochastic processes are discrete and, naturally, stochastic ones. In the same time they are used in many cases for modelling of the same real processes (as city traffic, epidermis and many others). They can reflect different aspects of modelling systems and can be good supplements each other; but their harmonisation is a separate complex problem. It would be very important to integrate the both approaches in one general approach. It is especially actual for researches on bioinformatics, when one deals with discrete data (like genome), but directs to describe and predict continuous effects on a macro level.

Within studies, devoted to combination of the two approaches, there are a number of articles, especially oriented to bioinformatics problems (Anderson, Chaplain, 1998). The work (Smilde, et al, 2015) shows a way to understand some potential stochastic features of biological systems on the base of their differential models. The authors used well-known covariance analysis to estimate variance in some biological indices. In the article (Mei et al, 2015), stochastic flows are directly built into the bioinformatics differential equations and can be used for processing web-based biological data through a web-interface of the model. Also an Internet-based tools for biological data processing, combined different modelling technique, including differential equations and stochastic processes, are proposed in (Yu et al, 2013).

To describe stochastic effects in biological systems, there are a number of approaches based on different computation methods (Tavassoly et al., 2018). Constructed computational algorithms can be distributed (Boczkowski et al., 2018) or realized as a special modeling tool (Azeloglu, Iyengar, 2015).

There are also a set of quite sophisticate models, based on ideas of differential calculus, w/hich describe some special discrete and stochastic effects in bioinformatics systems. In the paper (Azuma et al, 2007), discrete biochemical pathways are identifying using a special qualitative topologic analysis of corresponding differential equations. A “general model of biological change”, which consists of two equations and directs on use of small samples, is proposed in (Rasnick, 2009). The continuous model can help with description of discrete genetic pathways.

Interesting researches, which gave some ideas for the current study, took place in the field of using bioinformatics data and discrete approaches for development of adequate differential models of biological systems. The paper (Iba, 2008) with the speaking title “Inference of differential equation models by genetic programming” describes a way to improve differential biological models of the base of genetics methods.

Applied researches in the field of complex use of continuous and discrete/stochastic models, like in bioinformatics, can help in discovering new approaches in the theory of dynamical systems (Smitalova, Sujan, 1991; Hannon, Ruth, 1994). Thus, matching the two types of descriptions can support identification of system dynamical parameters (Holder, Rodrigo, 2013; Ballnus, 2017) or even specification of the system's structure (Shih, Parthasarathy, 2012).

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